

We Claim:

1. An isolated BTA nucleic acid molecule of at least 30 nucleotides which hybridizes to SEQ ID NO. 1, or the complement of SEQ ID NO. 1, under stringent hybridization conditions.
- 5 2. An isolated nucleic acid molecule which comprises:
 - (i) a nucleic acid sequence having substantial sequence identity or sequence similarity with a nucleic acid sequence of any one of SEQ. ID. NOs. 1 through 8;
 - (ii) nucleic acid sequences complementary to (i);
 - (iii) nucleic acid sequences differing from any of the nucleic acid sequences of (i) or (ii) in codon
10 sequences due to the degeneracy of the genetic code; or
 - (iv) a fragment, or allelic or species variation of (i), (ii) or (iii).
3. A vector comprising a nucleic acid molecule of claim 2.
4. A host cell comprising a nucleic acid molecule of claim 2.
5. A method for preparing a protein comprising:
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 - (a) transferring a vector as claimed in claim 3 into a host cell;
 - (b) selecting transformed host cells from untransformed host cells;
 - (c) culturing a selected transformed host cell under conditions which allow expression of the protein;
and
 - (d) isolating the protein.
- 20 6. A protein prepared in accordance with the method of claim 5.
7. An antibody having specificity against an epitope of a protein as claimed in claim 6.
8. An antibody as claimed in claim 7 labeled with a detectable substance and used to detect the protein in biological samples, tissues, and cells.
9. A method for detecting a nucleic acid molecule as claimed in claim 2 in a biological sample comprising
25 the steps of:
 - (a) hybridizing a nucleic acid molecule of claim 2 to nucleic acids of the biological sample, thereby forming a hybridization complex; and
 - (b) detecting the hybridization complex wherein the presence of the hybridization complex correlates with the presence of a nucleic acid molecule encoding the protein in the biological sample.
- 30 10. A method as claimed in claim 9 wherein nucleic acids of the biological sample are amplified by the polymerase chain reaction prior to the hybridizing step.
11. A method of diagnosing and monitoring cancer mediated by a tumor associated protein by determining the presence of a nucleic acid molecule encoding the tumor associated protein or the presence of the tumor associated protein wherein the tumor associated protein is protein phosphatase 4 regulatory
35 subunit (Genbank AJ271448); a protein product corresponding to Genbank AK001674; putative translation initiation factor (SUI1) (Genbank NM-005801); RNA helicase (Genbank AL359945); MIL1 protein, nuclear gene encoding mitochondrial protein (NM-015367); MacMarks protein (Genbank

X70326); chromosome 11 open reading frame 10 (c11orf10) (Genbank AF0867763); plakophilin 4 (PKP4) (Genbank NM-003628), or a protein encoded by the nucleic acid molecule as claimed in claim 2.

12. A method as claimed in claim 11 wherein the condition is breast cancer.

5 13. A method for preventing or treating a condition mediated by a tumor associated protein which is protein phosphatase 4 regulatory subunit (Genbank AJ271448); a protein product corresponding to Genbank AK001674; putative translation initiation factor (SUI1) (Genbank NM-005801); RNA helicase (Genbank AL359945); MIL1 protein, nuclear gene encoding mitochondrial protein (NM-015367); MacMarks protein (Genbank X70326); chromosome 11 open reading frame 10 (c11orf10) (Genbank
10 AF0867763); plakophilin 4 (PKP4) (Genbank NM-003628), or a protein encoded by the nucleic acid molecule as claimed in claim 2, comprising administering an effective amount of an antibody specific for the tumor associated protein.

14. A method as claimed in claim 13 wherein the cancer is breast cancer.

15 15. A vaccine to prevent cancer and/or to treat cancer comprising a tumor associated protein which is protein phosphatase 4 regulatory subunit (Genbank AJ271448); a protein product corresponding to Genbank AK001674; putative translation initiation factor (SUI1) (Genbank NM-005801); RNA helicase (Genbank AL359945); MIL1 protein, nuclear gene encoding mitochondrial protein (NM-015367); MacMarks protein (Genbank X70326); chromosome 11 open reading frame 10 (c11orf10) (Genbank
20 AF0867763); plakophilin 4 (PKP4) (Genbank NM-003628), or a protein encoded by the nucleic acid molecule as claimed in claim 2, or peptides derived from the protein, or synthetic peptides thereof, or any combination of these molecules.

16. A method to prevent cancer or to treat cancer in subjects who have a tumor associated protein on their cells comprising administering a vaccine for stimulating or enhancing in the subjects antibodies directed against the tumor associated protein wherein the tumor associated protein is protein phosphatase 4
25 regulatory subunit (Genbank AJ271448); a protein product corresponding to Genbank AK001674; putative translation initiation factor (SUI1) (Genbank NM-005801); RNA helicase (Genbank AL359945); MIL1 protein, nuclear gene encoding mitochondrial protein (NM-015367); MacMarks protein (Genbank X70326); chromosome 11 open reading frame 10 (c11orf10) (Genbank AF0867763); plakophilin 4 (PKP4) (Genbank NM-003628), or a protein encoded by the nucleic acid molecule as
30 claimed in claim 2.

17. A method for preventing patients from having tumors prior to their occurrence comprising administering a vaccine as claimed in claim 15.

18. A method for stimulating or enhancing in a subject production of antibodies directed against a tumor associated protein comprising administering to the subject a vaccine as claimed in claim 15 in a dose
35 effective for stimulating or enhancing production of the antibodies.

19. A methods for treating, preventing, or delaying recurrence of cancer comprising administering to the subject a vaccine as claimed in claim 15 in a dose effective for treating, preventing, or delaying

Figure 6. The effect of the number of iterations (n) on the accuracy of the proposed algorithm. The results are shown for different values of α and β . The x-axis represents the number of iterations (n), ranging from 0 to 100. The y-axis represents the error, ranging from 0 to 1. The legend indicates the following parameter combinations:

- $\alpha = 0.5, \beta = 0.5$ (Blue line)
- $\alpha = 0.7, \beta = 0.3$ (Orange line)
- $\alpha = 0.9, \beta = 0.1$ (Green line)
- $\alpha = 0.1, \beta = 0.9$ (Red line)

The graph shows that the error generally decreases as the number of iterations increases, with the rate of decrease depending on the chosen values of α and β .

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